DO NOT CONSIDER FOR TALK

2025 SEA Symposium Abstract

South Texas College

McAllen TX

Corresponding Faculty Member: Courtney Galle (cgalle@southtexascollege.edu)

Isolation and Characterization of two Microbacterium foliorum phages Losacky and Zahlia

Andrew Amdahl, Magdalena Diaz, Oscar Espinosa, Genesis Fuentes, Sean Gutierrez, Joshua Lopez, Joanna Martinez, Michelle Mejia, Sophia Morin, Randy Vela

Bacteriophages are viruses that specifically target and infect bacterial cells by injecting their DNA to replicate, ultimately killing the bacteria. They are crucial because they can be used to fight bacterial infections through phage therapy and vaccine development. Two novel viruses, Zahlia and Losacky, were isolated via enriched extraction from moist dirt samples collected from Edcouch and Mercedes, Texas, respectively using host *Microbacterium foliorum* NRRL B-24224. These viruses were purified through three rounds of plating at 30⁰C for 48 hours. After purification, genomic DNA from each was then sequenced at the University of Pittsburgh. Bacteriophage Zahlia is classified into cluster EE, a group of bacteriophages that share significant genetic similarities. It exhibits physical traits typical of the siphoviridae family. Zahlia’s genome is 17,481 base pairs in length, with a GC content of 68.8 percent. The bacteriophage, Losacky, is identified as a siphoviridae containing 38,622 base pairs. This phage belongs to the cluster GA and has a GC content of 68.1%. Interesting findings of this phage include a single tRNA gene, and no reverse genes identified. Analyzing bacteriophage genomes allows us to explore key aspects of gene structure, organization, regulation, and function, providing deeper insights into viral and bacterial interactions. This research is essential for understanding bacteriophage roles in bacterial ecology, developing phage therapies, and expanding our knowledge of molecular biology and evolution.